Data–driven Modelling of Intrinsically Disordered Proteins

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Propositions

accompanying the thesis

Data-driven Modelling of Intrinsically Disordered Proteins

by

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1. Chemical shifts of intrinsically disordered proteins can be predicted from their amino acid sequences. — Chapter 2
2. Chemical shift libraries compiled from chemically unfolded and short—length polypeptides are not representative of intrinsically disordered states. — Chapter 2
3. The ‘random—coil' term does not reflect the conformational preferences of peptide chains and should be used with great care. — Chapter 6
4. Numerical simulations based on experimental observations can be of fundamental importance for drawing inferences of how biochemical systems are organized, function, and are regulated.
5. Data—driven automation is the future of structural biochemistry.
6. Academic excellence is a multi—modal function of creativity, stubbornness and luck.
7. Open--access publishing and citizen science projects may avert the damage done by institutionalized pseudo—science and 'fake news' movements.